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FIG. 1A.

GACTACGTTGGTGTAGAAAAATCCTGCCGCCCGGACCCTTAAGGCTGGGACAAATTTCTGATAGCTACCCCGACACAGGAGGTTACGGGATGAGCA 95

M S

ATTCGGCCCGCGCTCACTCAGGTGGTCATGTTGCTGAGCGTGCTGGCTGCCGTGGGGCTGGCCACGGCGCCCGGCGGCCCGGCCCCG 190

SIGNAL SEQUENCE-----MTB32A
N S R R S L R W S L L S V L A A V G L G L A T A P A Q A A P

CGGCTTGTGCGCAGGACCGGTTCCCGCGCTTCCCGCGCTCGACCCCTCGCGGATGGTCCGCCAAGTGGGGCCACAGGTGGTCAACAT 285

MTB322A-----
P A L S Q D R F A D F P A L P L D P S A M V A Q V G P Q V V N I

CAACACCAAACCTGGCTACAAACGCGGTGGCGCGGACCGGCATCGTCATCGATCCCAACGGTGTCTGTGACCAACACCGTGATCG 380

MTB322A-----
N T K L G Y N N A V G A G T G I V I D P N G V V L T N N H V I

CGGGCCCAACGACATCAATGCGTTCAGCGTCCGGCTCCGGCCAAACCTACGGCGTCGATGTGGTCGGGTATGACCGCACCCAGGATGTGCGGGTG 475

MTB322A-----
A G A T D I N A F S V G S G Q T Y G V D V G Y D R T Q D V A V

CTGCAGCTGCCGGTGCCGCTGCCGTCCGGCGGATCGGTGGCGCGTCCGGTGGTGAGCCCGTCTGCGGATGGGCAACAGCGGTGG 570

MTB322A-----
L Q L R G A F F L P S A A I G G G V A V G E P V A M G N S G G

GCAGGGCGGAACGCCCGTGCGGTGCGTGGCAGGGTGGTCCGGCTCGGCCAAACCGTGCAGGGCGTCGGATTGCTGACCGGTGCCGAAGAGACAT 665

MTB322A-----
Q G G T P R A V P G R V V A L G Q T V Q A S D S L T G A E E T

TGAACGGTTGATCCAGTTCGATCCCGGATCCAGCCCGGTGATTCCGGCGGGCCCGTCTCAACGGCCCTAGCACAGGTGGTCCGGTATGAACACG 760

MTB322A-----
L N G L I Q F D A A I Q P G D S G G P V V N G L G Q V V G M N

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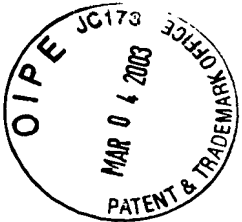
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GCCGCGTCCGATAACTCCAGCTGTCCAGGTGGCAGGGATTCCGCAATTCGGATCGGGCAGGCGATGGCGATCCGATCCGATCGGG 855
-----MTB322A-----
A A S D N F Q L S Q G G Q G F A I P I G Q A M A I A G Q I R S G
TGGGGGTCAACCCACCGTTTCATATCGGGCCTACCGCCTTCTCGGCTTGGGTGTGTCGACAACAACGGCAACGGCGACGAGTCCAACGCGTGG 950
-----MTB322A-----
G G S P T V H I G P T A F L G L G V V D N N G N F A R V Q R V
TCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTGATCACCGCGGTGACGGCGTCCGATCAACTCGGCCACCGCGATGGCG 1045
-----MTB322A-----
V G S A P A A S L G I S T G D V I T A V D G A P I N S A T A M A
GACGCGCTTAACGGGCGATCATCCCGGTGACGTCTCGGTGACCTGGCAAACCAAGTCGGGGCGGCACGCGTACAGGGAACGTGACATTGGCCGA 1140
-----MTB322A-----
D A L N G H H P G D V I S V T W Q T K S G G T R T G N V T L A 2/12
GGGACCCCGGCCTGATTTCGTGCGGGATACCAACCCCGCGCGGCAATTGGATTGGCGCCAGCCCGTATTGCCCGGTGAGCCCCCGAGTTCGG 1235
---MTB322A--->
E G P P A
TCTCCCGTGGCGTGGCATCGTGAAGCAATGAACGAGGCGAGAACACAGCGTCGAGCACCCCTCCCGTGCCAGGCGCAGTCACGTGCAAGGCGGTGTG 1330
GTCGAGCATCCGGATGCCAAGGACTTCGGCAGCGCCGCGCCCTGCCCGCGATCCGACCTGGTTAAGCACGCCGCTTCTACGAGGTGCTGGT 1425
CCGGCGGTCTTCGACGCCAGCGCGGACGGTTCGGCGATCTCGTGGAATCGATCGCCTCGACTACCTGCACTGAGTGGCTTGGCATCGACTGCA 1520
TCTGGTTGCCGCGCTTACGACTCGCCGCTGCGGACGGCGGTACGACATTCGCGACTTCTACAGGCTGTCGCCGAATTCGGCACCGTCGAC 1615
GATTTCGTCGCGCTGTCGACGCGCTCACCGGCGAGGTATCCGCATCATCACCGACCTGGTGATGAATCACACCTCGGAGTCGACCCCTGGTT 1710
TCAGGAGTCCCGCGGACCCAGACGCGTACGGTACTATTACGTGTGGAGCGACACCGAGCGGTACACCGACGCCCGGATCATCTTCG 1805
TCGACACCGAAGAGTCGAACCTGTCATTCGATCCTGTCCGCCGACAGTTCTACTGGCACCGGATTCTT 1872

FIG. 1B.

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ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGCAGGGATTCCGCATTCCGATCGGGCAGCGATGGCGA
-----Ra12-----
T A A S D N F Q L S Q G G Q G F A I P I G G A M A

TCGGGGCCAGATCCGGTGGGGGTACCCACCGTTCATATCGGGCCCTACCGCCTTCCTCGGCTTGGGTGTTGCGACAACACGGCAACGGCGC
-----Ra12-----
I A G Q I R S G G S P T V H I G P T A F L G L G V V D N N G N G A

ACGAGTCCAAACGCGTGGTCCGGGAGCGCTCCGGGGCAAGTCTCGGCATCTCCACCGCGGACGTGATCACCGCGGTGACGGCGCTCCGATCAACTCGGCC
-----Ra12-----
R V Q R V V G S A P A A S L G I S T G D V I T A V D G A P I N S A

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ACCGCATGGCGGACCGCTTAACGGGCATCATCCCGGTGACGTCACTCGGTGACCTGGCAACCAAGTCCGGCGGCACGCGTACAGGGAACGTGACAT
-----Ra12-----
T A M A D A L N G H P G D V I S V T W Q T K S G G T R T G N V T

TGGCCGAGGACCCCGGCC
-----Ra12-----
L A E G P P A

FIG. 2.

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CATATGCATCACCATCACACGGCCCGGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGGATTCCGCATTCCGATCGGGCAGGGCGAT 95
|-----Met (6xHis)-----|-----Ra12-----
M H H H H H H T A A S D N F Q L S Q G G Q F A I P I G Q A M
GGCGATCGGGGCCAGATCCGATCGGGGTGCGGGGTCAACCCACCGTTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAAACAACG 190
-----Ra12-----
A I A G Q I R S G G G S P T V H I G P T A F L G L G V D N N
GCAACGGCGCAGAGTCCAACGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGTGATCACCGCGGTGCGACGGCGCT 285
-----Ra12-----
G N G A R V Q R V V G S A P A A S L G I S T G O V I T A V D G A
CCGATCAACTCGGCCACCGGATGGCGGACGGCGCTTAACGGGCATCATCCCCGGTGACGTGACCTCGGTGACCTGGCAAACCAAGTCGGGGCGGCAC 380
-----Ra12-----
P I N S A T A M A D A L N G H H P G O V I S V T W Q T K S G G T
GCGTACAGGAACGTGACATTGGCCGAGGACCCCCGGCGAATTGACGACGACGACAAGGATCCACCTGACCCCGCATCAGCCGGACATGACGA 475
-----Ra12-----EcoR Enterokinase-----DPPD-----
R T G N V T L A E G P P A E F D D D K D P P D P H Q P D M T
AAGGCTATTGCCCCGGTGGCGATGGGGTTTGGCGACTTGGCCGTGTGCGACGGCGAGAAGTACCCGACGGCTCGTTTGGCACCAAGTGGATG 570
-----DPPD-----
K G Y C P G G R W G F G D L A V C D G E K Y P D G S F W H Q W M
CAAACGTGGTTTACCGGGCCACAGTTTACTTCGATTGTGTCAGCGCGGTGAGCCCCCTCCCGCGCCCGCCACCGGTGTTGCGGTGGGC 665
-----DPPD-----
Q T W F T G P Q F Y F D C V S G G E P L P G P P P G G C G G A
AATTCGTCGAGCAGCCCAACGCTCCCTGAGAATC
-----DPPD-----→
I P S E Q P N A P

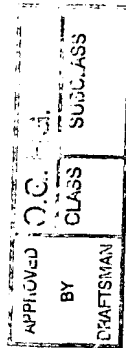
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FIG. 3.

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FIG. 4A.

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FIG. 4B.

CAAACAGGAACCGAGCTGGGTGGTGCAGAACCGCACGAAGACAGTGCCTGAGCGCATTCACCGTTCACTTCTCCGGCCAGTTCACTGGCACAG 760
-----WT1-----
K Q E P S W G G A E P H E E Q C L S A F T V H F S G Q F T G T
CGGAGCCTGTCGCTACGGGCCCTTCGGTCCCTCCGCCAGCCAGCGGTCCATCCGGCCAGGCCAGGATGTTCTTAACGGCCCTACCTGCC 855
-----WT1-----
A G A C R Y G P F G P P P S Q A S S G Q A R M F P N A P Y L P
AGTGCCTCGAGAGCCAGCCCGCTATTTCGCAATCAGGGTTACAGCACGGTCACTTCGACGGGACGCCAGCTACGGTCAACACGCCCTCGCACCA 950
-----WT1-----
S C L E S Q P A I R N Q G Y S T V T F D G T P S Y G H T P S H H
TGCGGCGAGTTCCCAACCACTCATTCAAGCATGAGGATCCCATGGCCAGCAGGGCTCGCTGGGTGAGCAGCAGTACTCGGTGCCGCCCGG 1045
-----WT1-----
A A Q F P N H S F K H E D P M G - Q G S L G E Q Q Y S V P P P
TCTATGGCTGCCACACCCACCGACAGCTGCACCGGCAGCCAGGCTTGTCTGCTAAGGACGCCCTACAGCAGTGACAATTATACCAATGACA 1140
-----WT1-----
V Y G C H T P T D S C T G S Q A L L R T P Y S S D N L Y Q M T
TCCCAGCTTGAATGCATGACCTGGAATCAGATGAACCTTAGGAGCCACCTTAAAGGGCCACAGCACAGGGTACGAGAGCGGATAACCCACACACGCC 1235
-----WT1-----
S Q L E C M T W N Q M N L G A T L K G H S T G Y E S D N H T T P
CATCCTCTCGGAGCCCAATACAGAATACACACCGGTGTCTTCAGAGGCATTACGATGTGCAACGTGTCCCTGGAGTAGCCCCGACTCTG 1330
-----WT1-----
I L C G A Q Y R I H T H G V F R G I Q D V A R V P G V A P T L

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TACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTTTCATGTGTGCTTACTCAGGCTGCAATAAGAGATAATTTAAGCTGTCCACTTACAGATG 1425
-----WT1-----
V R S A S E T S E K R P F M C A Y S G C N K R Y F K L S H L Q M

CACAGCAGGAAGCACACTGGTGAGAAACCATACCAGTGTGACTTCAAGGACTGTGAACGAAGGTTTTTTCGTTCAAACCCAGCTCAAAAGACACCA 1520
-----WT1-----
H S R K H T G E K P Y Q C D F K D C E R R F F R S D Q L K R H Q

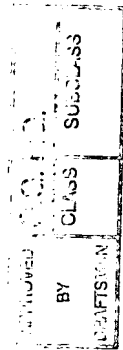
AAGGAGACATACAGGTGTGAACCATTCAGTGTAAACTTGTGAGCGAAAGTTCTCCCGTCCGACCACCTGAAGACCCACACCCAGGACTCATA 1615
-----WT1-----
R R H T G V K P F Q C K T C Q R K F S R S D H L K T A T R T H

CAGGTGAAAAGCCCTTCAGCTGTCCGGTGGCCAAAGTTGTCAGAAAAAGTTTGCCCGGTGAGATGAATTAGTCCGCCATCACAACATACATCAGAGA 1710
-----WT1-----
T G E K P F S C R W P S C Q K K F A R S D E L V R H H N M H Q R

AACATGACCAAACTCCAGCTGGCGCTTTGAGAATTC
-----WT1-----→
N M T K L Q L A L

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FIG. 4C.



CATATGCATCACCATCACACGGCCGGTCCGATAACTTCCAGCTGTCCAGGTGGCAGGGATTCCGATTCGGCAGGCGGAT 95
|-----Met (6xHis)-----|-----Ra12-----
M H H H H H H T A A S D N F Q L S Q G G Q G F A I P I G Q A M

GGCGATCGCGGCCAGATCCGATCGGGTGGGGGTCAACCCACCGTTTCATATCGGGCTACCGCCTTCCCTCGGCTTGGGTGTTGTCGACAAACG 190
-----Ra12-----
A I A G Q I R S G G G S P T V H I G P T A F L G L G V V D N N

GCAACGGCGACGAGTCCAACGCGTGGTGGGAGCGTCCGGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTGCGACGGCGCT 285
-----Ra12-----
G N G A R V Q R V V G S A P A A S L G I S T G O V I T A V D G A

CCGATCAACTCGGCCACCGCATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCTCGGTGACCTGGCAACCAAGTCGGGGCGGCAC 380
-----Ra12-----
P I N S A T A M A D A L N G H H P G O V I S V T W Q T K S G G T

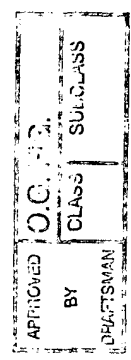
GCGTACAGGGAACGTGACATTGGCCGAGGACCCCGCCGGAATTTCATCGAGGGAAGGGCTCTGGCTGCCCTTATTGGAGAATGTGATTCCA 475
-----Ra12-----
R T G N V T L A E G P P A E F I E G R G S G C P L L E N V I S
|EcoR|Factor Xa|-----MAMMAGLOBIN-----

AGACAATCAATCCACAAGTGTCTAAGACTGAATACAAAGAACTTCTTCAAGAGTTCATAGACGACAATGCCACTACAAATGCCATAGATGAATTG 570
-----MAMMAGLOBIN-----
K T I N P Q V S K T E Y K E L L Q E F I D D N A T T N A I D E L

AAGGAATGTTTCTTAACCAACGGATGAAACTCTGAGCAATGTTGAGGTGTTTATGCAATTATATATACAGCAGCTTTGTGATTATTATA 665
-----MAMMAGLOBIN----->
K E C F L N Q T D E T L S N V E V F M Q L I Y D S S L C D L F

AGAATTC 672

FIG. 5.



ATGCATCACCATCACACGGCGCGTCCGATAACTTCCAGCTGTCCAGGTGGCAGGGATTCCGCATTCCGATCGGGCAGGCGGATGGC 95
-----Met (6xHis)-----Ra12-----
M H H H H H T A A S D N F Q L S Q G G Q G F A I P I G Q A M A

GATCGGGGCCAGATCCGATCGGGTGGGGGTACCCACCGTTCATATCGGGCCCTACCGCCTTCTCTCGGCTTGGGTGTGTCGACAACAACGGCA 190
-----Ra12-----
I A G Q I R S G G S P T V H I G P T A F L G L G V V D N N G

ACGGCGCAGAGTCCAAACGGCTGTCGGGAGCGCTCCGGGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCTGACGGCGCTCCG 285
-----Ra12-----
N G A R V Q R V V G S A P A A S L G I S T G O V I T A V D G A P

ATCAACTCGGCCACCGGATGGCGGACGCGCTTAACGGGCATCATCCGGTGACGTGACCTCGGTGACCTGGCAAAACCAAGTCGGGGCGCACGGC 380
-----Ra12-----
I N S A T A M A D A L N G H H P G O V I S V T W Q T K S G G T R

TACAGGAACTGACATGGCCGAGGACCCCGCGCAATTTCATGGTGATTTCGGGGCGTTACACCGGAGATCAACTCCCGGAGGATGTACG 475
-----Ra12-----EcoRI-----MTB39-----
T G N V T L A E G P P A E F M V D F G A L P P E I N S A R M Y

CCGGCCCGGCTCGCTGGTGGCCCGGCTCAGATGTGGGACAGCGTGGCGAGTGACCTGTTTCGGCCCGGTTCAGTCCGTG 570
-----MTB39-----
A G P G S A S L V A A A Q M W D S V A S D L F S A A S A F Q S V

GTCTGGGTCTGACGGTGGGTCTGATAGTTCTGTCGGCGGTCTGATGGTGGCGGCGCTCGCCGTATGTGCGTGGATGAGCGTCACCGC 665
-----MTB39-----
V W G L T V G S W I G S S A G L M V A A A S P Y V A W M S V T A

GGGCAGCCGAGCTGACCGCCCGAGTCCGGTTGCTGCGGGCGCTACGAGACGGCGTATGGGTGACGGTCCCCCGGTGATCGCCG 760
-----MTB39-----
G Q A E L T A A Q V R V A A A A Y E T A Y G L T V P P P V I A

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FIG. 6A.



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AGAACCGTGCTGAAGTATCTGATAGCGACCAACCTCTTGGGGCAAAACACACCCGGCGATCGCGGTCAACGAGGCCGAATACGGCGAGATG 855
-----MTB39-----
E N R A E L M I L I A T N L L G Q N T P A I A V N E A E Y G E M
TGGGCCCCAAGACGCCCGCGATGTTTGGCTACGCCCGCGGACGGCGGACGGCGGACGTTGCTGCCGTTTCGAGGAGGCCCGGAGATGAC 950
-----MTB39-----
W A Q D A A A M F G Y A A A T A T A T L L P F E E A P E M T
CAGCGGGGTGGCTCCTCGAGCAGGCCCGCGGTGAGGAGCCTCCGACACCCCGCGGGAACCAAGTTGATGAACAATGTCCCCAGGGCG 1045
-----MTB39-----
S A G G L L E Q A A A V E E A S D T A A A N Q L M N N V P Q A
TGCAACAGCTGGCCCGACGACGAGGCACCGCCTTCTTCAAGCTGGGTGGCCTGTGGAAGACGGTCTGCCCGCATCGGTCCGCGATCAGC 1140
-----MTB39-----
L Q Q L A Q P T Q G T T P S S K L G G L W K T V S P H R S P I S
AACATGTCGATGGCCCAACAACCATGTCGATGACCAACTCGGGTGTGTCGATGACCAACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCC 1235
-----MTB39-----
N M V S M A N N H M S M T N S G V S M T N T L S S M L K G F A P
GGCGGGCGCCCGCGTGCACCGCGGCGGCAAAACGGGGTCCGGGCGATGAGCTCGCTGGGCAGCTCGCTGGGTCTTTCGGGTCTGGGCG 1330
-----MTB39-----
A A A A Q A V Q T A A Q N G V R A M S S L G S S L G L G
GTGGGTGGCCGCAACTTGGGTGGCGGCGCTCGGTGCTGTCGTCGCGAGGCTGGCGCGGCAACCAAGCAGTCACCCCGCG 1425
-----MTB39-----
G G V A A N L G R A A S V G S L S V P Q A W A A A N Q A V T P A
GGCGGGCGCTGCCGTCACCAAGCGCGGAAAGAGGGCCCGGCGAGATGCTGGCGGGCTGCCGGTGGGCAGATGGCGGCCAG 1520
-----MTB39-----
A R A L P L T S L T S A A E R G P G Q M L G G L P V G D M G A R

FIG. 6B.

GGCCCGGTGGTGGGCTCAGTGCTGTGCTGCCTTCGGCGCACCCCTATGTATGATGCCGCAATTCTCCGGCAGCCGGCGATATCGCCCCCGCGGCCT 1611

A G G G L S G V L R V P P R P Y V M P H S P A A G D I A P P A Eco

TGTCGCAGGACCGGTTCCCGCGACTTCCCCCGGCTGCCCTCGACCCGTCGCGCATGGTCGCCCAAAGTGGGGCCACAGGTGGTCAACATCAACACC 1710

L S Q D R F A D F P A L P L D P S A M V A Q V G P Q V V N I N T MTB32A (N-ter)

AAACTGGGTACAACAACGCCGTGGGCGCGGACCGGCATCGTCATCGATCCC AACGGTGTCTGTCTGACCAACAACACGTCGATCGCGGGCGC 1805

K L G Y N N A V G A G T G I V I D P N G V V L T N N H V I A G A MTB32A (N-ter)

CACCGACATCAATGCGTTCAGCGTCGGCTCCGGCCAAACCTACGGCGTCGATGTGGTCGGGTATGACCGCACCCAGGATGTCCGGGTGCTGCAGC 1900

T D I N A F S V G S G Q T Y G V D V V G Y D R T Q D V A V L Q WT1

TGCGCGGTGCCCTGCCGTGCGCGGCGATCGGTGGCGCGTTCGGTGGAGCCCCGTCTGTCGGATGGGCAACAGCGGTGGGCAGGCG 1995

L R G A G G L P S A A I G G V A V G E P V A M G N S G G Q G MTB32A (N-ter)

GGAACGCCCGTGGGTGCCTGGCAGGGTGGTCGCGCTCGGCCAACCCGTGCAGGCGTCGGATTCTGCTGACCGGTGCCGAGAGACATTGAACGG 2090

G T P R A V P G R V V A L G Q T V Q A S D S L T G A E T L N G MTB32A (N-ter)

GTTGATCCAGTTCGATCCAGCCCGGTGATTTCGGGCGGCGCCGTCGTCAACGGCCTAGGACAGGTGGTTCGGTATGAACACGGCCGCGT 2185

L I O F D A A I O P G D S G G P V V N G L G O V V G M N T A A WT1

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Ra12(short) polypeptide (SEQ ID NO:17)

TAASDNFQLSQGGQGFPIPIGQAMAIAGQI

FIG. 7.

Ra12(long) polypeptide (SEQ ID NO: 18)

TAASDNFQLSQGGQGFPIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGARV
 QRVVGSAPAAASLGISTGDTVITAVDGAIPINSATAMADALNGHHPGDVISVTWQTKSG
 GTRTGNVTLAEGPPA

FIG. 8.

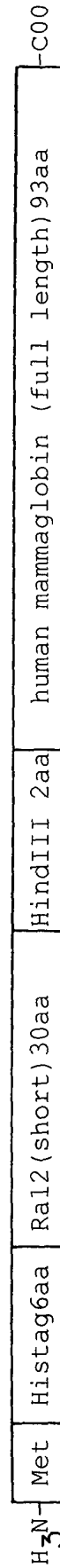


FIG. 9.